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☐ 1. Document ID: US 20070026505 A1

L6: Entry 1 of 3 File: PGPB Feb 1, 2007

PGPUB-DOCUMENT-NUMBER: 20070026505
PGPUB-FILING-TYPE:
DOCUMENT-IDENTIFIER: US 20070026505 A1

TITLE: Amino acid and metabolite biosynthesis

PUBLICATION-DATE: February 1, 2007

INVENTOR-INFORMATION:

NAME	CITY	STATE	COUNTRY
Madden; Kevin T.	Arlington	MA	US
Walbridge; Michael J.	Dorchester	MA	US
Yorgey; Peter S.	Cambridge	MA	US
Doten; Reed	Framingham	MA	US

US-CL-CURRENT: 435/106; 435/252.3, 435/252.33, 435/471

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | Claims | KWMC | Draw Desc | Image

☐ 2. Document ID: US 20050260721 A1

L6: Entry 2 of 3 File: PGPB Nov 24, 2005

PGPUB-DOCUMENT-NUMBER: 20050260721
PGPUB-FILING-TYPE: new
DOCUMENT-IDENTIFIER: US 20050260721 A1

TITLE: Method for zymotic production of fine chemicals (mety) containing sulphur

PUBLICATION-DATE: November 24, 2005

INVENTOR-INFORMATION:

NAME	CITY	STATE	COUNTRY
Kroger, Burkhard	Limburgerhof		DE
Zelder, Oskar	Speyer		DE
Klopproge, Corinna	Mannheim		DE
Schroder, Hartwig	Nussloch		DE
Hafner, Stefan	Ludwigshafen		DE

US-CL-CURRENT: 435/113; 435/252.3

☐ 3. Document ID: US 20050255568 A1

L6: Entry 3 of 3 File: PGPB Nov 17, 2005

PGPUB-DOCUMENT-NUMBER: 20050255568
PGPUB-FILING-TYPE: new
DOCUMENT-IDENTIFIER: US 20050255568 A1

TITLE: Methods and compositions for amino acid production

PUBLICATION-DATE: November 17, 2005

INVENTOR-INFORMATION:

NAME	CITY	STATE	COUNTRY
Bailey, Richard B.	South Natick	MA	US
Blomquist, Paul	Roslindale	MA	US
Doten, Reed	Framingham	MA	US
Driggers, Edward M.	Arlington	MA	US
Madden, Kevin T.	Arlington	MA	US
O'Leary, Jessica	Somerville	MA	US
O'Toole, George	Hanover	NH	US
Trueheart, Joshua	Concord	MA	US
Walbridge, Michael J.	Dorchester	MA	US
Yorgey, Peter S.	Cambridge	MA	US

US-CL-CURRENT: 435/113; 435/191, 435/193, 435/252.33

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | Claims | KWIC | Draw Desc | Image

Clear | Generate Collection | Print | Fwd Refs | Bkwd Refs | Generate OACS

Terms	Documents
Mycobacterium and O-acetylhomoserine sulfhydrolase	3

Display Format: - Change Format

Previous Page Next Page Go to Doc#

L7: Entry 4 of 8 File: PGPB Mar 24, 2005

PGPUB-DOCUMENT-NUMBER: 20050064551
PGPUB-FILING-TYPE: new
DOCUMENT-IDENTIFIER: US 20050064551 A1

TITLE: Nucleotide sequences which code for the metY gene

PUBLICATION-DATE: March 24, 2005

INVENTOR-INFORMATION:

NAME	CITY	STATE	COUNTRY
Moeckel, Bettina	Duesseldorf		DE
Pfefferle, Walter	Halle (Westf.)		DE
Huthmacher, Klaus	Gelnhausen		DE
Rueckert, Christian	Guetersloh		DE
Kalinowski, Joern	Bielefeld		DE
Puehler, Alfred	Bielefeld		DE
Binder, Michael	Steinhagen (Westf.)		DE
Greissinger, Dieter	Niddatal		DE
Thierbach, Georg	Bielefeld		DE

US-CL-CURRENT: 435/69.1; 435/196, 435/252.3, 435/320.1, 536/23.2

CLAIMS:

1-40. (Cancelled).

41. An isolated polynucleotide comprising: (a) a polynucleotide which encodes a polypeptide comprising the amino acid sequence of SEQ ID NO:2; or (b) a polynucleotide which hybridizes under stringent conditions to the complement of SEQ ID NO:1 and which encodes a protein with O-acetylhomoserine sulfhydrylase activity, wherein said stringent conditions comprises washing in 0.1.times.SSC at a temperature of from 50 to 68.degree. C.

42. The isolated polynucleotide of claim 41, which is (a).

43. The isolated polynucleotide of claim 41, which is (b).

44. A vector comprising the isolated polynucleotide of claim 42.

45. A vector comprising the isolated polynucleotide of claim 43.

46. A host cell comprising the isolated polynucleotide of claim 42.

47. The host cell of claim 46, which is a coryneform bacteria.

48. The host cell of claim 46, wherein the activity of the polypeptide encoded by the isolated polynucleotide is increased relative to the host cell without the isolated polynucleotide.

49. The host cell of claim 48, wherein the activity of the polypeptide is increased at least 10% relative to the host cell without the isolated polynucleotide.

50. A host cell comprising the isolated polynucleotide of claim 44.

51. The host cell of claim 50, which is a coryneform bacteria.

52. The host cell of claim 50, wherein the activity of the polypeptide encoded by the isolated polynucleotide is increased relative to the host cell without the isolated polynucleotide.

53. The host cell of claim 52, wherein the activity of the polypeptide is increased at least 10% relative to the host cell without the isolated polynucleotide.

54. A process for preparing L-amino acids, comprising culturing the host cell of claim 46 for a time and under conditions suitable for the production of the L-amino acid; and isolating the L-amino acid produced.

55. The process of claim 54, wherein the L-amino acid is L-lysine and/or L-methionine.

56. The process of claim 54, wherein the host cell comprises one or more overexpressed polynucleotides which encode a protein selected from the group consisting of glycerolaldehyde 3 phosphate dehydrogenase, triose phosphate isomerase, 3-phosphoglycerate kinase, pyruvate carboxylase, aspartate kinase, cystathionine-gamma-synthase, cystathionine-gamma-lyase- , and serine hydroxymethyltransferase.

57. The process of claim 54, wherein the host cell comprises one or more attenuated genes which encode proteins selected from the group consisting of phosphoenol pyruvate carboxykinase, glucose 6-phosphate isomerase, pyruvate oxidase, homoserine kinase, threonine dehydratase, threonine synthase, meso-diaminopimelate D-dehydrogenase, phosphoenol pyruvate carboxykinase, glucose 6-phosphate isomerase, and pyruvate oxidase.

58. A process for preparing L-amino acids, comprising culturing the host cell of claim 50 for a time and under conditions suitable for the production of the L-amino acid; and isolating the L-amino acid produced.

59. The process of claim 58, wherein the L-amino acid is L-lysine and/or L-methionine.

60. The process of claim 58, wherein the host cell comprises one or more overexpressed polynucleotides which encode a protein selected from the group consisting of glycerolaldehyde 3 phosphate dehydrogenase, triose phosphate isomerase, 3-phosphoglycerate kinase, pyruvate carboxylase, aspartate kinase, cystathionine-gamma-synthase, cystathionine-gamma-lyase- , and serine hydroxymethyltransferase.

61. The process of claim 58, wherein the host cell comprises one or more attenuated genes which encode proteins selected from the group consisting of phosphoenol pyruvate carboxykinase, glucose 6-phosphate isomerase, pyruvate oxidase, homoserine kinase, threonine dehydratase, threonine synthase, meso-diaminopimelate D-dehydrogenase, phosphoenol pyruvate carboxykinase, glucose 6-phosphate isomerase, and pyruvate oxidase.

62. A method of preparing an L-amino acid containing feedstuff additive, comprising (a) culturing the host cell of claim 46 in a fermentation broth for a time and under conditions suitable for the production of the L-amino acid; (b) concentrating the L-amino acid produced; (c) removing an amount of 0 to 100 wt % of biomass formed during the culturing; and (d) drying the fermentation broth obtained in one or both of (b) and (c) to obtain the animal feedstuff additive.

63. A method of preparing an L-amino acid containing feedstuff additive, comprising (a) culturing the host cell of claim 50 in a fermentation broth for a time and under conditions

L7: Entry 6 of 8 File: USPT Nov 2, 2004

US-PAT-NO: 6812016
DOCUMENT-IDENTIFIER: US 6812016 B2

TITLE: Nucleotide sequences which code for the metY gene

DATE-ISSUED: November 2, 2004

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
Moeckel; Bettina	Duesseldorf			DE
Pfefferle; Walter	Halle			DE
Huthmacher; Klaus	Gelnhausen			DE
Rueckert; Christian	Guetersloh			DE
Kalinowski; Joern	Bielefeld			DE
Puehler; Alfred	Bielefeld			DE
Binder; Michael	Steinhagen			DE
Greissinger; Dieter	Niddatal			DE
Thierbach; Georg	Bielefeld			DE

US-CL-CURRENT: 435/195; 435/106, 435/183, 435/252.33, 435/320.1, 435/6, 536/23.1, 536/23.2, 536/23.7

CLAIMS:

What is claimed is:

1. An isolated polynucleotide which comprises SEQ ID NO:1.

2. A vector comprising the isolated polynucleotide of claim 1.

3. A host cell comprising the isolated polynucleotide of claim 1.

4. The host cell of claim 3, which is a coryneform bacteria.

5. The host cell of claim 3, wherein the activity of the polypeptide encoded by the isolated polynucleotide is increased relative to the host cell without the isolated polynucleotide.

6. The host cell of claim 5, wherein the activity of the polypeptide is increased at least 10% relative to the host cell without the isolated polynucleotide.

7. A process for preparing L-amino acids, comprising culturing the host cell of claim 3 for a time and under conditions suitable for the production of the L-amino acid; and isolating the L-amino acid produced.

8. The process of claim 7, wherein the L-amino acid is L-lysine and/or L-methionine.

9. The process of claim 7, wherein the host cell comprises one or more overexpressed polynucleotides which encode a protein selected from the group consisting of glycerolaldehyde 3-phosphate dehydrogenase, triose phosphate isomerase, 3-phosphoglycerate kinase, pyruvate carboxylase, aspartate kinase, cystathionine-gamma-synthase, cystathionine-gamma-lyase, and serine hydroxymethyltransferase.

10. The process of claim 7, wherein the host cell comprises one or more attenuated genes which encode proteins selected from the group consisting of phosphoenol pyruvate carboxykinase, glucose 6-phosphate isomerase, pyruvate oxidase, homoserine kinase, threonine dehydratase, threonine synthase, meso-diaminopimelate D-dehydrogenase.

11. A method of preparing an L-amino acid containing feedstuff additive, comprising (a) culturing the host cell of claim 3 in a fermentation broth for a time and under conditions suitable for the production of the L-amino acid; (b) concentrating the L-amino acid produced; (c) removing an amount of 0 to 100 wt % of biomass formed during the culturing; and (d) drying the fermentation broth obtained in one or both of (b) and (c) to obtain the animal feedstuff additive.

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DATE: Tuesday, May 08, 2007

Hide?	Set Name	Query	Hit Count
		DB=PGPB,USPT,USOC,EPAB,JPAB,DWPI; PLUR=YES; OP=ADJ	
☐	L7	bacterium and O-acetylhomoserine sulfhydrolase	8
☐	L6	Mycobacterium and O-acetylhomoserine sulfhydrolase	3
☐	L5	Mycobacterium same O-acetylhomoserine sulfhydrolase	1
☐	L4	Mycobacterium tuberculosis same O-acetylhomoserine sulfhydrolase	0
		DB=USPT; PLUR=YES; OP=ADJ	
☐	L3	5965391	3
		DB=PGPB,USPT,USOC,EPAB,JPAB,DWPI; PLUR=YES; OP=ADJ	
☐	L2	Mycobacterium tuberculosis same MetY	3
		DB=USPT; PLUR=YES; OP=ADJ	
☐	L1	Mycobacterium tuberculosis same MetY	0

END OF SEARCH HISTORY

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=> s Mycobacterium and O-acetylhomoserine sulfhydrolase
L1            2 MYCOBACTERIUM AND O-ACETYLHOMOSERINE SULFHYDROLASE

=> dup rem l1
PROCESSING COMPLETED FOR L1
L2            2 DUP REM L1 (0 DUPLICATES REMOVED)

=> d l2 1-2 ibib ab

L2  ANSWER 1 OF 2  HCAPLUS  COPYRIGHT 2007 ACS on STN
ACCESSION NUMBER:         2006:148971  HCAPLUS
DOCUMENT NUMBER:          144:231584
TITLE:                    Production of L-cysteine or L-methione by genetically
                          engineered strains of Corynebacterium glutamicum
INVENTOR(S):              Sauer, Uwe; Mampel, Joerg; Schroeder, Hartwig;
                          Haefner, Stefan; Zelder, Oskar; Herold, Andrea;
                          Klopprogge, Corinna
PATENT ASSIGNEE(S):       BASF A.-G., Germany
SOURCE:                   Ger. Offen., 50 pp.
                          CODEN: GWXXBX
DOCUMENT TYPE:            Patent
LANGUAGE:                 German
FAMILY ACC. NUM. COUNT:   1
PATENT INFORMATION:

     PATENT NO.           KIND   DATE        APPLICATION NO.          DATE
     ---------------      ----   --------    --------------------     --------
     DE 102004035052       A1    20060216    DE 2004-102004035052     20040720
     WO 2006008152         A1    20060126    WO 2005-EP7925           20050720
         W:  AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BW, BY, BZ, CA, CH,
             CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, EG, ES, FI, GB, GD,
             GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KM, KP, KR, KZ,
             LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NA,
             NG, NI, NO, NZ, OM, PG, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK,
             SL, SM, SY, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU,
             ZA, ZM, ZW
         RW: AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HU, IE,
             IS, IT, LT, LU, LV, MC, NL, PL, PT, RO, SE, SI, SK, TR, BF, BJ,
             CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG, BW, GH,
             GM, KE, LS, MW, MZ, NA, SD, SL, SZ, TZ, UG, ZM, ZW, AM, AZ, BY,
             KG, KZ, MD, RU, TJ, TM
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EP 1769080 A1 20070404 EP 2005-773106 20050720
R: AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HU, IE, IS, IT, LI, LT, LU, LV, MC, NL, PL, PT, RO, SE, SI, SK, TR
PRIORITY APPLN. INFO.: DE 2004-102004035052A 20040720
WO 2005-EP7925 W 20050720

AB The present invention provides strains of Corynebacterium glutamicum that are enhanced for the prodn. of L-cysteine or L-methione. Specifically, the invention provides mutant strains of Corynebacterium glutamicum in which one or more transcription factor genes has been disrupted.

L2 ANSWER 2 OF 2 BIOTECHDS COPYRIGHT 2007 THE THOMSON CORP. on STN
ACCESSION NUMBER: 2004-12616 BIOTECHDS
TITLE: Fermentative production of sulfur-containing fine chemicals, useful e.g. as feed additive, by culturing bacteria containing heterologous sequence for O-acetylhomoserine sulfhydrolase;
L-amino acid production via bacterium fermentation for use in food industry
AUTHOR: KROEGER B; ZELDER O; KLOPPROGGE C; SCHROEDER H; HAEFNER S
PATENT ASSIGNEE: BASF AG
PATENT INFO: DE 10239082 4 Mar 2004
APPLICATION INFO: DE 2002-1039082 26 Aug 2002
PRIORITY INFO: DE 2002-1039082 26 Aug 2002; DE 2002-1039082 26 Aug 2002
DOCUMENT TYPE: Patent
LANGUAGE: German
OTHER SOURCE: WPI: 2004-228741 [22]

AB DERWENT ABSTRACT:
NOVELTY - Method for fermentative production of at least one sulfur-containing fine chemical (I) by fermenting a (I)-producing coryneform bacterium (A); concentrating (I) in medium or cells, then isolating it. (A) expresses at least one heterologous nucleotide sequence (II) that encodes a protein (III) with O-acetylhomoserine-sulfhydrolase (metY) activity.

DETAILED DESCRIPTION - An INDEPENDENT CLAIM is also included for preparation of a feed additive (B) that contains L-methionine by culturing/fermenting an L-Met producing microorganisms; removing water from the fermentation broth and optionally also up to 100% of the biomass, then drying the treated broth to recover (B) in powdered or granular form.

WIDER DISCLOSURE - This describes metY sequences (Z) from 27 specified microorganisms, and their functional homologs and the proteins encoded by them. All sequences are reproduced, e.g. for Corynebacterium diphtheriae ATCC 14779, a 1317 bp and 438 amino acid sequences. Also included are (a) fragments of (Z) that can be used as probes or primers for identification and cloning of homologous sequences, and (b) sequences that hybridize to, or are complementary to, (Z).

BIOTECHNOLOGY - Preferred Process: This is preparation of L-methionine by fermenting Corynebacterium glutamicum at 15-45, preferably 25-40, degreesC and pH 5-8.5, preferably 7, for 10-160 hours. Preferred Microorganisms: (A) contains a plasmid carrying at least one copy of (II), under control of regulatory sequences and is a strain in which (II) is overexpressed. Optionally (A) has at least one other gene (X) in the biosynthetic pathway to (I) amplified or mutated in such a way that its activity is not affected by metabolites, and/or at least one metabolic pathway that reduces formation of (I) is at least partly switched off. 15 (X) are specified, e.g. lysC (aspartate kinase); gap (glyceraldehyde-3-phosphate dehydrogenase); pgk (3-phosphoglycerate kinase); pyc (pyruvate carboxylase) and tpi (triosephosphate isomerase); also 10 genes e.g. thrB (homoserine kinase), ilvA (threonine dehydratase); thrC (threonine synthase) or ddh (meso-diaminopimelate D-dehydrogenase) that are reduced in activity, by changing the expression rate or by mutation. Preferred Nucleic Acid: (II) is less than 100% homologous with the sequence from C. glutamicum ATCC 13032 and is especially from any of 27 specified microorganisms, e.g. C. diphtheriae ATCC 14779; Mycobacterium tuberculosis ATCC 25584;

Saccharomyces cerevisiae ATCC 2704 or Candida albicans ATCC 10231. The metY sequences for all 27 species are reproduced, together with the sequences of the encoded enzymes, e.g. e.g. for Corynebacterium diphtheriae ATCC 14779, 1317 bp and 438 amino acid sequences. (II) is replicable in (A); DNA stably integrated into the chromosome or it is RNA. Isolation: (II) are isolated by establishing a gene library from the appropriate organism, then sequencing the fragments. Once isolated they are cloned into vectors for (over)expression, e.g. into pCLiK5MCS.

USE - The method is specifically used to prepare L-methionine or feed additives that contain it (claimed). More generally, (I) are useful in the food, feed, cosmetic and pharmaceutical industries.

ADVANTAGE - The method improves production of (I) (no more details).

EXAMPLE - No relevant examples are given. (134 pages)

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=> s corynebacterium and  O-acetylhomoserine sulfhydrolase
L3          11 CORYNEBACTERIUM AND O-ACETYLHOMOSERINE SULFHYDROLASE

=> dup rem l3
PROCESSING COMPLETED FOR L3
L4            6 DUP REM L3 (5 DUPLICATES REMOVED)

=> s corynebacterium and  sulfur compounds
L5          37 CORYNEBACTERIUM AND SULFUR COMPOUNDS

=> dup rem l5
PROCESSING COMPLETED FOR L5
L6           20 DUP REM L5 (17 DUPLICATES REMOVED)

=> s l6 and sulfur amino acid?
L7            0 L6 AND SULFUR AMINO ACID?

=> s l6 and methionine
L8            5 L6 AND METHIONINE

=> d l8 1-5 ibib ab

L8   ANSWER 1 OF 5     MEDLINE on STN
ACCESSION NUMBER:   2003247712     MEDLINE
DOCUMENT NUMBER:    PubMed ID: 12770504
TITLE:              The putative transcriptional repressor McbR, member of the
                    TetR-family, is involved in the regulation of the metabolic
                    network directing the synthesis of sulfur containing amino
                    acids in Corynebacterium glutamicum.
AUTHOR:             Rey Daniel Alexander; Puhler Alfred; Kalinowski Jorn
CORPORATE SOURCE:   Lehrstuhl fur Genetik, Universitat Bielefeld,
                    Universitatsstrasse 25, D-33501 Bielefeld, Germany.
SOURCE:             Journal of biotechnology, (2003 Jun 12) Vol. 103, No. 1,
                    pp. 51-65.
                    Journal code: 8411927. ISSN: 0168-1656.
PUB. COUNTRY:       Netherlands
DOCUMENT TYPE:      Journal; Article; (JOURNAL ARTICLE)
                    (RESEARCH SUPPORT, NON-U.S. GOV'T)
LANGUAGE:           English
FILE SEGMENT:       Priority Journals
ENTRY MONTH:        200404
ENTRY DATE:         Entered STN: 29 May 2003
                    Last Updated on STN: 21 Apr 2004
                    Entered Medline: 20 Apr 2004
AB   In order to isolate transcriptional regulatory proteins involved in L-
     methionine-dependent repression in Corynebacterium
     glutamicum, proteins binding to the putative promoter region upstream of
     the metY gene were isolated by DNA affinity chromatography. One of the
     isolated proteins was identified as a putative transcriptional repressor
     of the TetR-family by a mass spectrometry fingerprint technique based on
```

the complete C. glutamicum genome sequence. The respective gene, designated mcbR, was deleted in the mutant strain C. glutamicum DR1. Using 2D-PAGE, the protein contents of the C. glutamicum wild type and the mutant strain DR1 grown in media with or without L-methionine supplementation were compared and a set of six proteins was identified. Their abundance was drastically enhanced in the mutant strain and no longer influenced by L-methionine added to the growth medium. The corresponding genes were identified by mass spectrometry fingerprint analysis. They included metY encoding O-acetyl-L-homoserine sulfhydrylase, metK encoding S-adenosyl-methionine synthethase, hom encoding homoserine dehydrogenase, cysK encoding L-cysteine synthase, cysI encoding an NADPH dependant sulfite reductase, and ssuD encoding an alkanesulfonate monooxygenase. Evidently, the putative transcriptional repressor McbR is involved in the regulation of the metabolic network directing the synthesis of L-methionine in C. glutamicum. The C. glutamicum mcbR mutant can be considered to represent a first step in the construction of an L-methionine production strain.

L8 ANSWER 2 OF 5 MEDLINE on STN
ACCESSION NUMBER: 2002218281 MEDLINE
DOCUMENT NUMBER: PubMed ID: 11954798
TITLE: Production of volatile compounds by cheese-ripening yeasts: requirement for a methanethiol donor for S-methyl thioacetate synthesis by Kluyveromyces lactis.
AUTHOR: Arfi K; Spinnler H E; Tache R; Bonnarme P
CORPORATE SOURCE: Institut National de la Recherche Agronomique, Laboratoire de Genie et Microbiologie des Procedes Alimentaires, Thiverval-Grignon, France.
SOURCE: Applied microbiology and biotechnology, (2002 Mar) Vol. 58, No. 4, pp. 503-10. Electronic Publication: 2002-02-01. Journal code: 8406612. ISSN: 0175-7598.
PUB. COUNTRY: Germany: Germany, Federal Republic of
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE) (RESEARCH SUPPORT, NON-U.S. GOV'T)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200210
ENTRY DATE: Entered STN: 17 Apr 2002
Last Updated on STN: 5 Jan 2003
Entered Medline: 24 Oct 2002

AB Five cheese-ripening yeasts (Geotrichum candidum, Saccharomyces cerevisiae, Kluyveromyces lactis, Yarrowia lipolytica and Debaryomyces hansenii) were compared with respect to their ability to generate volatile aroma compounds. K. lactis produced a variety of esters - ethylacetate (EA) being the major one - and relatively limited amounts of volatile sulphur compounds (VSCs). Conversely, G. candidum produced significant amounts of VSCs [with the thioester S-methyl thioacetate (MTA) being the most prevalent] and lower quantities of non-sulphur volatile compounds than K. lactis. We suspect that K. lactis is able to produce and/or accumulate acetyl CoA - a common precursor of MTA and EA - but that it produces limited amounts of methanethiol (MTL); both acetyl CoA and MTL are precursors for MTA synthesis. When supplemented with exogenous MTL, MTA production greatly increased in K. lactis cultures whereas it was unchanged in G. candidum cultures, suggesting that MTL is a limiting factor for MTA synthesis in K. lactis but not in G. candidum. Our results are discussed with respect to L-methionine catabolism.

L8 ANSWER 3 OF 5 MEDLINE on STN
ACCESSION NUMBER: 2002195923 MEDLINE
DOCUMENT NUMBER: PubMed ID: 11928962
TITLE: L-methionine degradation potentialities of cheese-ripening microorganisms.
AUTHOR: Bonnarme P; Lapadatescu C; Yvon M; Spinnler H E
CORPORATE SOURCE: Institut National de la Recherche Agronomique, Laboratoire de Genie et Microbiologie des Procedes Alimentaires,

Thiverval-Grignon, France.. bonnarme@grignon.inra.fr
SOURCE: The Journal of dairy research, (2001 Nov) Vol. 68, No. 4, pp. 663-74.
Journal code: 2985125R. ISSN: 0022-0299.
PUB. COUNTRY: England: United Kingdom
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
(RESEARCH SUPPORT, NON-U.S. GOV'T)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200208
ENTRY DATE: Entered STN: 4 Apr 2002
Last Updated on STN: 31 Aug 2002
Entered Medline: 30 Aug 2002

AB Volatile sulphur compounds are major flavouring compounds in many traditional fermented foods including cheeses. These compounds are products of the catabolism of L-methionine by cheese-ripening microorganisms. The diversity of L-methionine degradation by such microorganisms, however, remains to be characterized. The objective of this work was to compare the capacities to produce volatile sulphur compounds by five yeasts, Geotrichum candidum, Yarrowia lipolytica, Kluyveromyces lactis, Debaryomyces hansenii, Saccharomyces cerevisiae and five bacteria, Brevibacterium linens, Corynebacterium glutamicum, Arthrobacter sp., Micrococcus lutens and Staphylococcus equorum of technological interest for cheese-ripening. The ability of whole cells of these microorganisms to generate volatile sulphur compounds from L-methionine was compared. The microorganisms produced a wide spectrum of sulphur compounds including methanethiol, dimethylsulfide, dimethyldisulfide, dimethyltrisulfide and also S-methylthioesters, which varied in amount and type according to strain. Most of the yeasts produced methanethiol, dimethylsulfide, dimethyldisulfide and dimethyltrisulfide but did not produce S-methylthioesters, apart from G. candidum that produced S-methyl thioacetate. Bacteria, especially Arth. sp. and Brevi. linens, produced the highest amounts and the greatest variety of volatile sulphur compounds includling methanethiol, sulfides and S-methylthioesters, e.g. S-methyl thioacetate, S-methyl thiobutyrate, S-methyl thiopropionate and S-methyl thioisovalerate. Cell-free extracts of all the yeasts and bacteria were examined for the activity of enzymes possibly involved in L-methionine catabolism, i.e. L-methionine demethiolase, L-methionine aminotransferase and L-methionine deaminase. They all possessed L-methionine demethiolase activity, while some (K. lactis, Deb. hansenii, Arth. sp., Staph. equorum) were deficient in L-methionine aminotransferase, and none produced L-methionine deaminase. The catabolism of L-methionine in these microorganisms is discussed.

L8 ANSWER 4 OF 5 MEDLINE on STN
ACCESSION NUMBER: 2001120785 MEDLINE
DOCUMENT NUMBER: PubMed ID: 11097940
TITLE: Diversity of L-methionine catabolism pathways in cheese-ripening bacteria.
AUTHOR: Bonnarme P; Psoni L; Spinnler H E
CORPORATE SOURCE: Laboratoire de Genie et Microbiologie des Procedes Alimentaires, Institut National de la Recherche Agronomique, Centre de Biotechnologies Argo-Industrielles, 78850 Thiverval-Grignon, France.. bonnarme@grignon.inra.fr
SOURCE: Applied and environmental microbiology, (2000 Dec) Vol. 66, No. 12, pp. 5514-7.
Journal code: 7605801. ISSN: 0099-2240.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200102
ENTRY DATE: Entered STN: 22 Mar 2001

Last Updated on STN: 22 Mar 2001
Entered Medline: 15 Feb 2001

AB Enzymatic activities that could be involved in methanethiol generation in five cheese-ripening bacteria were assayed, and the major sulfur compounds produced were identified. L-Methionine and alpha-keto-gamma-methyl-thio-butyric acid demethiolating activities were detected in whole cells and cell extracts (CFEs) of all the bacteria tested. No L-methionine deaminase activity could be detected in any of the ripening bacteria and L-methionine aminotransferase was detected in CFEs of Brevibacterium linens, Micrococcus luteus, and Corynebacterium glutamicum. The results suggest that several pathways for L-methionine catabolism probably coexist in these ripening bacteria.

L8 ANSWER 5 OF 5 HCAPLUS COPYRIGHT 2007 ACS on STN
ACCESSION NUMBER: 1996:454004 HCAPLUS
DOCUMENT NUMBER: 125:107367
TITLE: Degradation and desulfurization of dibenzothiophene sulfone and other sulfur compounds by Agrobacterium MC501 and a mixed culture
AUTHOR(S): Constanti, Magda; Giralt, Jaume; Bordons, Albert
CORPORATE SOURCE: Dep. de Bioquimica i Biotechnol., Univ. Rovira i Virgili, Catalonia, Spain
SOURCE: Enzyme and Microbial Technology (1996), 19(3), 214-219
CODEN: EMTED2; ISSN: 0141-0229
PUBLISHER: Elsevier
DOCUMENT TYPE: Journal
LANGUAGE: English
OTHER SOURCE(S): CASREACT 125:107367
AB Agrobacterium MC501 and the mixed culture composed of Agrobacterium MC501, Xanthomonas MC701, Corynebacterium sp. MC401, and Corynebacterium sp. MC402, all previously isolated from a coal mine area by an enrichment culture with dibenzothiophene (DBT), were used to study DBT sulfone desulfurization. Both cultures were able to use DBT sulfone as a sole source of sulfur for growth. This compd. was metabolized to 2-hydroxybiphenyl (2PP) and sulfate. Agrobacterium MC501 and the mixed culture could also utilize a wide range of org. and inorg. sulfur compds. as sources of sulfur such ad DBT, thianthrene, di-Ph sulfide, thiophene-2-carboxylate, di-Bu sulfide, methionine, cysteine, sulfate, and sulfite. Based on these results, the above-mentioned strains can be used to characterize and study coal desulfurization.

=> s sulfur containing fine chemical?
L9 6 SULFUR CONTAINING FINE CHEMICAL?

=> dup rem l9
PROCESSING COMPLETED FOR L9
L10 5 DUP REM L9 (1 DUPLICATE REMOVED)

=> s l10 and bacterium
L11 3 L10 AND BACTERIUM

=> d l11 1-3 ibib ab

L11 ANSWER 1 OF 3 BIOTECHDS COPYRIGHT 2007 THE THOMSON CORP. on STN
ACCESSION NUMBER: 2004-12617 BIOTECHDS
TITLE: Fermentative production of sulfur-containing fine chemicals, useful e.g. as feed additive, by culturing bacteria containing heterologous sequence for methionine synthase; L-methionine production via bacterium culture for use in food and pharmaceutical industry
AUTHOR: KROEGER B; ZELDER O; KLOPPROGGE C; SCHROEDER H; HAEFNER S

PATENT ASSIGNEE: BASF AG
PATENT INFO: DE 10239308 11 Mar 2004
APPLICATION INFO: DE 2002-1039308 27 Aug 2002
PRIORITY INFO: DE 2002-1039308 27 Aug 2002; DE 2002-1039308 27 Aug 2002
DOCUMENT TYPE: Patent
LANGUAGE: German
OTHER SOURCE: WPI: 2004-228762 [22]
AB DERWENT ABSTRACT:
NOVELTY - Fermentative production of at least one sulfur-containing fine chemical (I) by fermenting a (I)-producing coryneform bacterium (A), concentrating (I) in medium or cells, then isolating it. (A) expresses at least one heterologous nucleotide sequence (II) that encodes a protein (III) with methionine synthase (metF) activity.

DETAILED DESCRIPTION - An INDEPENDENT CLAIM is also included for preparation of a feed additive (B) that contains L-methionine by culturing/fermenting an L-Met producing microorganisms, removing water from the fermentation broth and optionally also up to 100 % of the biomass, then drying the treated broth to recover (B) in powdered or granular form.

WIDER DISCLOSURE - This describes metF sequences (Z) from 26 specified microorganisms, and their functional homologs and the proteins encoded by them. All sequences are reproduced, e.g. for Corynebacterium diphtheriae ATCC 14779, 984 base pairs and 327 amino acid sequences. Also included are fragments of (Z) that can be used as probes or primers for identification and cloning of homologous sequences, and sequences that hybridize to, or are complementary to, (Z).

BIOTECHNOLOGY - Preferred Process: This is preparation of L-methionine by fermenting Corynebacterium glutamicum at 15-45, preferably 25-40, degreesC and pH 5-8.5, preferably 7, for 10-160 hours. Preferred Microorganisms: (A) contains a plasmid carrying at least one copy of (II), under control of regulatory sequences and is a strain in which (II) is overexpressed. Optionally (A) has at least one other gene (X) in the biosynthetic pathway to (I) amplified or mutated in such a way that its activity is not affected by metabolites, and/or at least one metabolic pathway that reduces formation of (I) is at least partly switched off. 15 (X) are specified, e.g. lysC (aspartate kinase); gap (glyceraldehyde-3-phosphate dehydrogenase); pgk (3-phosphoglycerate kinase); pyc (pyruvate carboxylase) and tpi (triosephosphate isomerase); also 10 genes e.g. thrB (homoserine kinase), ilvA (threonine dehydratase); thrC (threonine synthase) or ddh (meso-diaminopimelate D-dehydrogenase) that are reduced in activity, by changing the expression rate or by mutation. Preferred Nucleic Acid: (II) is less than 100 % homologous with the sequence from C. glutamicum ATCC 13032 and is especially from any of 26 specified microorganisms, e.g. C. diphtheriae ATCC 14779; Streptomyces lividans ATCC 19844; Saccharomyces cerevisiae ATCC 10751 or Vibrio cholerae ATCC 39315. The metF sequences for all 26 species are reproduced, together with the sequences of the encoded enzymes, e.g. for Corynebacterium diphtheriae ATCC 14779, 984 base pairs and 327 amino acid sequences. (II) is replicable in (A), DNA stably integrated into the chromosome or it is RNA. Isolation: (II) are isolated by establishing a gene library from the appropriate organism, then sequencing the fragments. Once isolated they are cloned into vectors for (over)expression, e.g. into pCLiK5MCS.

USE - The method is specifically used to prepare L-methionine or feed additives that contain it (claimed). More generally, (I) are useful in the food, feed, cosmetic and pharmaceutical industries.

ADVANTAGE - The method improves production of (I).

EXAMPLE - No relevant examples are given.(97 pages)

L11 ANSWER 2 OF 3 BIOTECHDS COPYRIGHT 2007 THE THOMSON CORP. on STN
ACCESSION NUMBER: 2004-12616 BIOTECHDS
TITLE: Fermentative production of sulfur-containing fine chemicals, useful e.g. as feed additive, by culturing bacteria containing

heterologous sequence for O-acetylhomoserine sulfhydrolase; L-amino acid production via bacterium fermentation for use in food industry

AUTHOR: KROEGER B; ZELDER O; KLOPPROGGE C; SCHROEDER H; HAEFNER S
PATENT ASSIGNEE: BASF AG
PATENT INFO: DE 10239082 4 Mar 2004
APPLICATION INFO: DE 2002-1039082 26 Aug 2002
PRIORITY INFO: DE 2002-1039082 26 Aug 2002; DE 2002-1039082 26 Aug 2002
DOCUMENT TYPE: Patent
LANGUAGE: German
OTHER SOURCE: WPI: 2004-228741 [22]

AB DERWENT ABSTRACT:

NOVELTY - Method for fermentative production of at least one sulfur-containing fine chemical (I) by fermenting a (I)-producing coryneform bacterium (A); concentrating (I) in medium or cells, then isolating it. (A) expresses at least one heterologous nucleotide sequence (II) that encodes a protein (III) with O-acetylhomoserine-sulfhydrolase (metY) activity.

DETAILED DESCRIPTION - An INDEPENDENT CLAIM is also included for preparation of a feed additive (B) that contains L-methionine by culturing/fermenting an L-Met producing microorganisms; removing water from the fermentation broth and optionally also up to 100% of the biomass, then drying the treated broth to recover (B) in powdered or granular form.

WIDER DISCLOSURE - This describes metY sequences (Z) from 27 specified microorganisms, and their functional homologs and the proteins encoded by them. All sequences are reproduced, e.g. for Corynebacterium diphtheriae ATCC 14779, a 1317 bp and 438 amino acid sequences. Also included are (a) fragments of (Z) that can be used as probes or primers for identification and cloning of homologous sequences, and (b) sequences that hybridize to, or are complementary to, (Z).

BIOTECHNOLOGY - Preferred Process: This is preparation of L-methionine by fermenting Corynebacterium glutamicum at 15-45, preferably 25-40, degreesC and pH 5-8.5, preferably 7, for 10-160 hours. Preferred Microorganisms: (A) contains a plasmid carrying at least one copy of (II), under control of regulatory sequences and is a strain in which (II) is overexpressed. Optionally (A) has at least one other gene (X) in the biosynthetic pathway to (I) amplified or mutated in such a way that its activity is not affected by metabolites, and/or at least one metabolic pathway that reduces formation of (I) is at least partly switched off. 15 (X) are specified, e.g. lysC (aspartate kinase); gap (glyceraldehyde-3-phosphate dehydrogenase); pgk (3-phosphoglycerate kinase); pyc (pyruvate carboxylase) and tpi (triosephosphate isomerase); also 10 genes e.g. thrB (homoserine kinase), ilvA (threonine dehydratase); thrC (threonine synthase) or ddh (meso-diaminopimelate D-dehydrogenase) that are reduced in activity, by changing the expression rate or by mutation. Preferred Nucleic Acid: (II) is less than 100% homologous with the sequence from C. glutamicum ATCC 13032 and is especially from any of 27 specified microorganisms, e.g. C. diphtheriae ATCC 14779; Mycobacterium tuberculosis ATCC 25584; Saccharomyces cerevisiae ATCC 2704 or Candida albicans ATCC 10231. The metY sequences for all 27 species are reproduced, together with the sequences of the encoded enzymes, e.g. e.g. for Corynebacterium diphtheriae ATCC 14779, 1317 bp and 438 amino acid sequences. (II) is replicable in (A); DNA stably integrated into the chromosome or it is RNA. Isolation: (II) are isolated by establishing a gene library from the appropriate organism, then sequencing the fragments. Once isolated they are cloned into vectors for (over)expression, e.g. into pCLiK5MCS.

USE - The method is specifically used to prepare L-methionine or feed additives that contain it (claimed). More generally, (I) are useful in the food, feed, cosmetic and pharmaceutical industries.

ADVANTAGE - The method improves production of (I) (no more details).

EXAMPLE - No relevant examples are given. (134 pages)

ACCESSION NUMBER: 2004-12478 BIOTECHDS
TITLE: Fermentative production of sulfur-containing fine chemicals, useful e.g. as feed additive, by culturing bacteria containing heterologous sequence for homoserine O-acetyltransferase; L-methionine production via bacterium fermentation for use in food and pharmaceutical industry
AUTHOR: KROEGER B; ZELDER O; KLOPPROGGE C; SCHROEDER H; HAEFNER S
PATENT ASSIGNEE: BASF AG
PATENT INFO: DE 10239073 11 Mar 2004
APPLICATION INFO: DE 2002-1039073 26 Aug 2002
PRIORITY INFO: DE 2002-1039073 26 Aug 2002; DE 2002-1039073 26 Aug 2002
DOCUMENT TYPE: Patent
LANGUAGE: German
OTHER SOURCE: WPI: 2004-240693 [23]

AB DERWENT ABSTRACT:

NOVELTY - Method for fermentative production of at least one sulfur-containing fine chemical (I) by fermenting a (I)-producing coryneform bacterium (A); concentrating (I) in medium or cells, then isolating it. (A) expresses at least one heterologous nucleotide sequence (II) that encodes a protein (III) with homoserine O-acetyltransferase (metA) activity.

DETAILED DESCRIPTION - An INDEPENDENT CLAIM is also included for preparation of a feed additive (B) that contains L-methionine by culturing/fermenting an L-Met producing microorganisms; removing water from the fermentation broth and optionally also up to 100% of the biomass, then drying the treated broth to recover (B) in powdered or granular form.

WIDER DISCLOSURE - Also disclosed are metA sequences (Z) from 23 specified microorganisms, and their functional homologs and the proteins encoded by them. All sequences are reproduced, e.g. for Corynebacterium diphtheriae ATCC 14779, 1104 bp and 367 amino acid sequences. Also disclosed are: (a) fragments of (Z) that can be used as probes or primers for identification and cloning of homologous sequences; and (b) sequences that hybridize to, or are complementary to, (Z).

BIOTECHNOLOGY - Preferred Process: This is preparation of L-methionine by fermenting Corynebacterium glutamicum at 15-45, preferably 25-40, degreesC and pH 5-8.5, preferably 7, for 10-160 hours. Preferred Microorganisms: (A) contains a plasmid carrying at least one copy of (II), under control of regulatory sequences and is a strain in which (II) is overexpressed. Optionally (A) has at least one other gene (X) in the biosynthetic pathway to (I) amplified or mutated in such a way that its activity is not affected by metabolites, and/or at least one metabolic pathway that reduces formation of (I) is at least partly switched off. 15 (X) are specified, e.g. lysC (aspartate kinase); gap (glyceraldehyde-3-phosphate dehydrogenase); pgk (3-phosphoglycerate kinase); pyc (pyruvate carboxylase) and tpi (triosephosphate isomerase); also 10 genes e.g. thrB (homoserine kinase), ilvA (threonine dehydratase); thrC (threonine synthase) or ddh (meso-diaminopimelate D-dehydrogenase) that are reduced in activity, by changing the expression rate or by mutation. Preferred Nucleic Acid: (II) is less than 100% homologous with the sequence from C. glutamicum ATCC 13032 and is especially from any of 23 specified microorganisms, e.g. C. diphtheriae ATCC 14779; Mycobacterium tuberculosis ATCC 25584; Saccharomyces cerevisiae ATCC 10751 or Schizosaccharomyces pombe ATCC 24969. The metA sequences for all these species are reproduced, together with the sequences of the encoded enzymes, e.g. for Corynebacterium diphtheriae ATCC 14779, 1104 bp and 367 amino acid sequences. (II) is replicable in (A); DNA stably integrated into the chromosome or it is RNA. Isolation: (II) are isolated by establishing a gene library from the appropriate organism, then sequencing the fragments. Once isolated they are cloned into vectors for (over)expression, e.g. into pCLiK5MCS (5091 bp sequence reproduced).

USE - The method is specifically used to prepare L-methionine or feed additives that contain it (claimed). More generally, (I) are useful

in the food, feed, cosmetic and pharmaceutical industries.
ADVANTAGE - The method improves production of (I) (no more details).
EXAMPLE - No relevant examples are given. (96 pages)

```
=> s l6 and Mycobacterium
L12          0 L6 AND MYCOBACTERIUM

=> focus l6
PROCESSING COMPLETED FOR L6
L13          20 FOCUS L6 1-

=> d l6 1-5

L6   ANSWER 1 OF 20  BIOSIS  COPYRIGHT (c) 2007 The Thomson Corporation  on STN
AN   2005:428286  BIOSIS
DN   PREV200510226623
TI   Methods in Biotechnology.
AU   Barredo, JL [Editor]
SO   Barredo, JL [Editor]. (2005) Methods in Biotechnology.
     Publisher: HUMANA PRESS INC, 999 RIVERVIEW DR, STE 208, TOTOWA, NJ
     07512-1165 USA. Series: METHODS IN BIOTECHNOLOGY.
     ISBN: 1-58829-548-6(H).
DT   Book
LA   English
ED   Entered STN: 26 Oct 2005
     Last Updated on STN: 26 Oct 2005

L6   ANSWER 2 OF 20  BIOSIS  COPYRIGHT (c) 2007 The Thomson Corporation  on STN
AN   2006:54102  BIOSIS
DN   PREV200600044401
TI   Functional genomics and expression analysis of the Corynebacterium
     glutamicum fpr2-cysIXHDNYZ gene cluster involved in assimilatory sulphate
     reduction.
AU   Rueckert, Christian; Koch, Daniel J.; Rey, Daniel A.; Albersmeier,
     Andreas; Mormann, Sascha; Puehler, Alfred; Kalinowski, Joern [Reprint
     Author]
CS   Univ Bielefeld, Inst Genomforsch, D-33594 Bielefeld, Germany
     cruecker@genetik.uni-bielefeld.de; dkoch@genetik.uni-bielefeld.de;
     daniel.rey@genetik.uni-bielefeld.de; aalbersm@genetik.uni-bielefeld.de;
     smormann@genetik.uni-bielefeld.de; puehler@genetik.uni-bielefeld.de;
     joern.kalinowski@genetik.uni-bielefeld.de
SO   BMC Genomics, (SEP 13 2005) Vol. 6.
     ISSN: 1471-2164.
DT   Article
LA   English
ED   Entered STN: 4 Jan 2006
     Last Updated on STN: 4 Jan 2006

L6   ANSWER 3 OF 20     MEDLINE on STN                    DUPLICATE 1
AN   2006754978     MEDLINE
DN   PubMed ID: 17191896
TI   3-Methyl-3-sulfanylhexan-1-ol as a major descriptor for the human
     axilla-sweat odour profile.
AU   Troccaz Myriam; Starkenmann Christian; Niclass Yvan; van de Waal Matthijs;
     Clark Anthony J
CS   Firmenich SA, Corporate R&D Division, P.O. Box 239, CH-1211 Geneva 8.
SO   Chemistry & biodiversity, (2004 Jul) Vol. 1, No. 7, pp. 1022-35.
     Journal code: 101197449. E-ISSN: 1612-1880.
CY   Switzerland
DT   Journal; Article; (JOURNAL ARTICLE)
LA   English
FS   Priority Journals
EM   200702
ED   Entered STN: 29 Dec 2006
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Last Updated on STN: 20 Feb 2007
Entered Medline: 19 Feb 2007

L6 ANSWER 4 OF 20 MEDLINE on STN DUPLICATE 2
AN 2005260141 MEDLINE
DN PubMed ID: 15900740
TI Desulfurization of dibenzothiophene by a newly isolated Corynebacterium sp. ZD-1 in aqueous phase.
AU Wang Miao-Dong; Li Wei; Wang Da-Hui; Shi Yao
CS Department of Environmental Engineering, Zhejiang University, Hangzhou 310027, China.
SO Journal of environmental sciences (China), (2004) Vol. 16, No. 6, pp. 1011-5.
Journal code: 100967627. ISSN: 1001-0742.
CY Netherlands
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 200507
ED Entered STN: 20 May 2005
Last Updated on STN: 20 Jul 2005
Entered Medline: 19 Jul 2005

L6 ANSWER 5 OF 20 MEDLINE on STN
AN 2003247712 MEDLINE
DN PubMed ID: 12770504
TI The putative transcriptional repressor McbR, member of the TetR-family, is involved in the regulation of the metabolic network directing the synthesis of sulfur containing amino acids in Corynebacterium glutamicum.
AU Rey Daniel Alexander; Puhler Alfred; Kalinowski Jorn
CS Lehrstuhl fur Genetik, Universitat Bielefeld, Universitatsstrasse 25, D-33501 Bielefeld, Germany.
SO Journal of biotechnology, (2003 Jun 12) Vol. 103, No. 1, pp. 51-65.
Journal code: 8411927. ISSN: 0168-1656.
CY Netherlands
DT Journal; Article; (JOURNAL ARTICLE)
(RESEARCH SUPPORT, NON-U.S. GOV'T)
LA English
FS Priority Journals
EM 200404
ED Entered STN: 29 May 2003
Last Updated on STN: 21 Apr 2004
Entered Medline: 20 Apr 2004

=> s l6 and MetY
L14 1 L6 AND METY

=> s l6 and metY
L15 1 L6 AND METY

=> d l15

L15 ANSWER 1 OF 1 MEDLINE on STN
AN 2003247712 MEDLINE
DN PubMed ID: 12770504
TI The putative transcriptional repressor McbR, member of the TetR-family, is involved in the regulation of the metabolic network directing the synthesis of sulfur containing amino acids in Corynebacterium glutamicum.
AU Rey Daniel Alexander; Puhler Alfred; Kalinowski Jorn
CS Lehrstuhl fur Genetik, Universitat Bielefeld, Universitatsstrasse 25, D-33501 Bielefeld, Germany.
SO Journal of biotechnology, (2003 Jun 12) Vol. 103, No. 1, pp. 51-65.

Journal code: 8411927. ISSN: 0168-1656.
CY Netherlands
DT Journal; Article; (JOURNAL ARTICLE)
(RESEARCH SUPPORT, NON-U.S. GOV'T)
LA English
FS Priority Journals
EM 200404
ED Entered STN: 29 May 2003
Last Updated on STN: 21 Apr 2004
Entered Medline: 20 Apr 2004

=> d l15 ab

L15 ANSWER 1 OF 1 MEDLINE on STN
AB In order to isolate transcriptional regulatory proteins involved in L-methionine-dependent repression in Corynebacterium glutamicum, proteins binding to the putative promoter region upstream of the metY gene were isolated by DNA affinity chromatography. One of the isolated proteins was identified as a putative transcriptional repressor of the TetR-family by a mass spectrometry fingerprint technique based on the complete C. glutamicum genome sequence. The respective gene, designated mcbR, was deleted in the mutant strain C. glutamicum DR1. Using 2D-PAGE, the protein contents of the C. glutamicum wild type and the mutant strain DR1 grown in media with or without L-methionine supplementation were compared and a set of six proteins was identified. Their abundance was drastically enhanced in the mutant strain and no longer influenced by L-methionine added to the growth medium. The corresponding genes were identified by mass spectrometry fingerprint analysis. They included metY encoding O-acetyl-L-homoserine sulfhydrylase, metK encoding S-adenosyl-methionine synthethase, hom encoding homoserine dehydrogenase, cysK encoding L-cysteine synthase, cysI encoding an NADPH dependant sulfite reductase, and ssuD encoding an alkanesulfonate monooxygenase. Evidently, the putative transcriptional repressor McbR is involved in the regulation of the metabolic network directing the synthesis of L-methionine in C. glutamicum. The C. glutamicum mcbR mutant can be considered to represent a first step in the construction of an L-methionine production strain.

=> d his

(FILE 'HOME' ENTERED AT 11:12:56 ON 08 MAY 2007)

FILE 'MEDLINE, HCAPLUS, BIOSIS, BIOTECHDS, SCISEARCH, EMBASE' ENTERED AT 11:13:36 ON 08 MAY 2007

L1 2 S MYCOBACTERIUM AND O-ACETYLHOMOSERINE SULFHYDROLASE
L2 2 DUP REM L1 (0 DUPLICATES REMOVED)
L3 11 S CORYNEBACTERIUM AND O-ACETYLHOMOSERINE SULFHYDROLASE
L4 6 DUP REM L3 (5 DUPLICATES REMOVED)
L5 37 S CORYNEBACTERIUM AND SULFUR COMPOUNDS
L6 20 DUP REM L5 (17 DUPLICATES REMOVED)
L7 0 S L6 AND SULFUR AMINO ACID?
L8 5 S L6 AND METHIONINE
L9 6 S SULFUR CONTAINING FINE CHEMICAL?
L10 5 DUP REM L9 (1 DUPLICATE REMOVED)
L11 3 S L10 AND BACTERIUM
L12 0 S L6 AND MYCOBACTERIUM
L13 20 FOCUS L6 1-
L14 1 S L6 AND METY
L15 1 S L6 AND METY

=> log y
COST IN U.S. DOLLARS SINCE FILE ENTRY TOTAL SESSION

FULL ESTIMATED COST	49.26	49.47
DISCOUNT AMOUNTS (FOR QUALIFYING ACCOUNTS)	SINCE FILE ENTRY	TOTAL SESSION
CA SUBSCRIBER PRICE	-1.56	-1.56

STN INTERNATIONAL LOGOFF AT 11:23:15 ON 08 MAY 2007